

301 DSTAVALNRREEDFPATETIEBPSKODKPLIEKLAIIYVNSSFYKETAELHOLSGGEKCKK 360  
301 DSTAVALNRREEDFPATETIEBPSKODKPLIEKLAIIYVNSSFYKETAELHOLSGGEKCKK 360  
361 ITVPEKISYTTSPFCHOLRWKRSKSPKOLLGNPOASIAQIIVTVVLGVIGALYFGKNDK 420  
361 ITVPEKISYTTSPFCHOLRWKRSKSPKOLLGNPOASIAQIIVTVVLGVIGALYFGKNDK 420  
421 TGIORRAGVLPFLTNOCSSVSVAELFVVEKKLFPIHEIYSGYRVSSYFGLKLSDDL 480  
421 TGIORRAGVLPFLTNOCSSVSVAELFVVEKKLFPIHEIYSGYRVSSYFGLKLSDDL 480  
481 MRMLPSIIFTCIYVFMGLKPKADAFVFMFTLMVAVASASSMALAIAGOSVSVATLL 540  
481 MRMLPSIIFTCIYVFMGLKPKADAFVFMFTLMVAVASASSMALAIAGOSVSVATLL 540  
541 MTICVFPMIIFSGLLVNLTTIASWLSWLOQFSIPRYGFTALOHNEFLGONFCPGLNATGN 600  
541 MTICVFPMIIFSGLLVNLTTIASWLSWLOQFSIPRYGFTALOHNEFLGONFCPGLNATGN 600  
601 NPCNATCTGGEYLVKQIDISPMGLMKHVALACMIVIFLTIAVLKLLFLKCKS 655  
601 NPCNATCTGGEYLVKQIDISPMGLMKHVALACMIVIFLTIAVLKLLFLKCKS 655

## RESULT 2

US-09-245-808-1  
Sequence 1, Application US/09245808  
Patent No. 6313277  
GENERAL INFORMATION:  
APPLICANT: Doyle, L. Austin  
APPLICANT: Robs, Douglas D.  
APPLICANT: Abduzo, Lynne V.  
TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which  
FILE REFERENCE: encodes it  
CURRENT APPLICATION NUMBER: US/09/245,808  
CURRENT FILING DATE: 1999-02-05  
EARLIER APPLICATION NUMBER: 60/073763  
EARLIER FILING DATE: 1998-02-05  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 1  
LENGTH: 655  
TYPE: PRT  
ORGANISM: Human MCF-7/AdrVP cells  
US-09-245-808-1

Query Match 99.4%; Score 3331; DB 4; Length 655;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 651; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
1 MSSSNTVEFIPVQSGNTGFPATVSDLKAFTEGAVLSFHNICRYVTKSGFLPCKPYE 60  
1 MSSSNTVEFIPVQSGNTGFPATVSDLKAFTEGAVLSFHNICRYVTKSGFLPCKPYE 60  
61 KEILSNINGIMKPGALNAILGPTGGKSSLLDVLAARKDPSGLSGDVLINGAPPPANPKCN 120  
61 KEILSNINGIMKPGALNAILGPTGGKSSLLDVLAARKDPSGLSGDVLINGAPPPANPKCN 120  
121 SGVVOODVVMGTLVRENLOFSAALRLATTMTNHEKNERINVIIEELGLDKVADSKVGT 180  
121 SGVVOODVVMGTLVRENLOFSAALRLATTMTNHEKNERINVIIEELGLDKVADSKVGT 180  
181 QTRGVSGGRKRTSIGMELITDPSILSLDEPTTGLDSSSTANAVLLKXMSKGRITIF 240  
181 QTRGVSGGRKRTSIGMELITDPSILSLDEPTTGLDSSSTANAVLLKXMSKGRITIF 240  
241 SIHQPRYSIFKLFDLSLTLLASGRIMFGPQOALGYFESAGHCENYNNADFFLDIING 300  
241 SIHQPRYSIFKLFDLSLTLLASGRIMFGPQOALGYFESAGHCENYNNADFFLDIING 300

301 DSTAVALNRREEDFPATETIEBPSKODKPLIEKLAIIYVNSSFYKETAELHOLSGGEKCKK 360  
301 DSTAVALNRREEDFPATETIEBPSKODKPLIEKLAIIYVNSSFYKETAELHOLSGGEKCKK 360  
361 ITVPEKISYTTSPFCHOLRWKRSKSPKOLLGNPOASIAQIIVTVVLGVIGALYFGKNDK 420  
361 ITVPEKISYTTSPFCHOLRWKRSKSPKOLLGNPOASIAQIIVTVVLGVIGALYFGKNDK 420  
421 TGIORRAGVLPFLTNOCSSVSVAELFVVEKKLFPIHEIYSGYRVSSYFGLKLSDDL 480  
421 TGIORRAGVLPFLTNOCSSVSVAELFVVEKKLFPIHEIYSGYRVSSYFGLKLSDDL 480  
481 MRMLPSIIFTCIYVFMGLKPKADAFVFMFTLMVAVASASSMALAIAGOSVSVATLL 540  
481 MRMLPSIIFTCIYVFMGLKPKADAFVFMFTLMVAVASASSMALAIAGOSVSVATLL 540  
541 MTICVFPMIIFSGLLVNLTTIASWLSWLOQFSIPRYGFTALOHNEFLGONFCPGLNATGN 600  
541 MTICVFPMIIFSGLLVNLTTIASWLSWLOQFSIPRYGFTALOHNEFLGONFCPGLNATGN 600  
601 NPCNATCTGGEYLVKQIDISPMGLMKHVALACMIVIFLTIAVLKLLFLKCKS 655  
601 NPCNATCTGGEYLVKQIDISPMGLMKHVALACMIVIFLTIAVLKLLFLKCKS 655

## RESULT 3

US-09-134-001C-5561  
Sequence 5561, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucelle-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 5561  
LENGTH: 270  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-5561

Query Match 7.2%; Score 241; DB 4; Length 270;  
Best Local Similarity 27.1%; Pred. No. 1,48-16;  
Matches 81; Conservative 55; Mismatches 103; Indels 60; Gaps 12;  
42 ICYRYKL-----KSGFLPC-----RKPEKILSNINGIMKPG-LNALIGPTG 83  
42 ICYRYKL-----KSGFLPC-----RKPEKILSNINGIMKPG-LNALIGPTG 83  
84 GGSKSLDLVLAARKDPSGLSGDVLING--APPAN-----FKCSGVVODVVMGTLT 135  
84 GGSKSLDLVLAARKDPSGLSGDVLING--APPAN-----FKCSGVVODVVMGTLT 135  
61 SKRTLLVAVSSIDVMT--KSGITINGKQELSKQJSDIRKQIDIGFIDQYVNLTLT 118  
61 SKRTLLVAVSSIDVMT--KSGITINGKQELSKQJSDIRKQIDIGFIDQYVNLTLT 118  
136 VRENTQFSAALRLATTMTNHEKNERINVIIEELGLDKVADSKVGTQFTRGVSGGRKRTS 195  
136 VRENTQFSAALRLATTMTNHEKNERINVIIEELGLDKVADSKVGTQFTRGVSGGRKRTS 195  
119 VENTIMLPASVQDKQIMH--ERYORIVELANTSDLS-----KYSSELGSGGRKRTS 170  
119 VENTIMLPASVQDKQIMH--ERYORIVELANTSDLS-----KYSSELGSGGRKRTS 170  
196 IGMELITDPSILSLDEPTTGLDSSSTANAVLLKXMSKGRITIFSIHQPRYSIFKLPD 254  
196 IGMELITDPSILSLDEPTTGLDSSSTANAVLLKXMSKGRITIFSIHQPRYSIFKLPD 254  
171 AARAFINPSIIFADBPGLADSKSLDLKRLKTMNEFNTTILMTHTDPAASFS--N 228  
171 AARAFINPSIIFADBPGLADSKSLDLKRLKTMNEFNTTILMTHTDPAASFS--N 228  
255 SLTLLASGRIMFGPQOALGYFESAGHCENYNNAD--FFLDIINGDSTAVALNR 310  
255 SLTLLASGRIMFGPQOALGYFESAGHCENYNNAD--FFLDIINGDSTAVALNR 310  
229 RVVMLKDGQIF-----TELQGDDBDKQTYKKEIIRTQSVLGGINYE 269  
229 RVVMLKDGQIF-----TELQGDDBDKQTYKKEIIRTQSVLGGINYE 269

## RESULT 4

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2003, 18:38:41 ; Search time 24.5012 Seconds

(without alignments)  
1257.181 Million cell updates/sec

Title: US-09-856-927-2

Perfect score: 3350

Sequence: 1 MSSSNVEFIPVSGNTNGF.....MIVFLTAYLKLPLKXYS 655

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3344	99.8	655	1	ABG2_HUMAN
2	1786.5	53.3	650	1	ABG1_MOUSE
3	835.5	24.9	1049	1	ADP1_YEAST
4	803	24.0	687	1	WHIT_DROME
5	762.5	22.8	679	1	WHIT_CERCA
6	748.5	22.3	677	1	WHIT_LUCIF
7	745	22.2	695	1	WHIT_ANOGA
8	730.5	21.8	709	1	WHIT_ANOGA
9	712.5	21.3	666	1	ABG1_MOUSE
10	704.5	21.0	678	1	ABG1_HUMAN
11	702	21.0	646	1	ABG4_HUMAN
12	690.5	20.6	652	1	ABG5_MOUSE
13	678.5	20.3	652	1	ABG5_MOUSE
14	676.5	20.2	598	1	ABG5_RAT
15	674.5	20.1	651	1	ABG5_HUMAN
16	671	20.0	672	1	ABG8_RAT
17	664	19.8	673	1	ABG8_MOUSE
18	653.5	19.5	1294	1	YOH5_YEAST
19	649.5	19.4	666	1	SCRT_DROME
20	637.5	19.0	673	1	ABG8_HUMAN
21	618.5	18.5	610	1	YOSC_CAEEL
22	605.5	18.1	1501	1	SNQ2_YEAST
23	603	18.0	1501	1	BFR1_SCHPO
24	601.5	18.0	1499	1	CDR2_CANAL
25	596	17.8	1511	1	PDR3_YEAST
26	588	17.6	1564	1	PDR3_YEAST
27	579	17.3	1333	1	YN99_YEAST
28	569	17.0	1529	1	PDR2_YEAST
29	537	16.0	1501	1	CDR3_CANAL
30	530.5	15.8	1501	1	CDR3_CANAL
31	527.5	15.7	1511	1	PDR3_YEAST
32	501	15.0	1430	1	CDR4_CANAL
33	483.5	14.4	1410	1	PDR8_YEAST

34	464	13.9	675	1	BROW_DROME
35	445	13.3	668	1	BROW_DROVI
36	237	7.1	355	1	CYGA_SYNY2
37	236.5	7.1	1704	1	ABG3_HUMAN
38	236	7.0	246	1	NATA_BACSU
39	236	7.0	371	1	MAUK_ECOLI
40	236	7.0	1321	1	AB11_HUMAN
41	235.5	7.0	236	1	LIVF_ARCFU
42	232.5	6.9	607	1	HEPA_ANASP
43	227	6.8	1302	1	MDR4_DROME
44	225.5	6.7	576	1	CYDC_HAEIN
45	224	6.7	347	1	NOD1_RHIGA

## ALIGNMENTS

RESULT 1  
ID ABG2\_HUMAN STANDARD; PRT; 655 AA.  
AC 09UNQ0; 095344; 09BY73; 09UN50;  
DT 16-OCT-2001 Rel. 40. Created)  
DT 28-FEB-2003 Rel. 41. Last sequence update)  
DE ATP-binding cassette, sub-family G, member 2 (placenta-specific ATP-binding cassette transporter) (Breast cancer resistance protein).  
GN ABG2 OR ABCP OR BCRP OR BCRPL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC TISSUE=Placenta;  
RP  
SEQUENCE FROM N.A.  
RC MEDLINE=99065313; PubMed=9850061;  
RA Allikmeets R., Schriml L.M., Hutchinson A., Romano-Spica V., Dean M.;  
RT "A human placenta-specific ATP-binding cassette gene (ABCP) on chromosome 4q22 that is involved in multidrug resistance.";  
RL Cancer Res. 58:5337-5339(1998).  
RN [2]  
RC SEQUENCE FROM N.A.  
RC TISSUE=Breast cancer;  
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,  
RT "A multidrug resistance transporter from human MCF-7 breast cancer cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:15665-15670(1998).  
RN [3]  
RC ERAP1.  
RA Doyle L.A., Yang W., Abruzzo L.V., Krogmann T., Gao Y., Rishi A.K.,  
RT "Proc. Natl. Acad. Sci. U.S.A. 96:2569-2569(1999)."  
RN [4]  
RC SEQUENCE FROM N.A.  
RA Kage M., Teukahara S., Sugiyama T., Asada S., Ishikawa E., Teurto T.,  
RT "Breast cancer resistance protein constitutes a 140-kDa complex as a homodimer.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RC SEQUENCE OF 198-655 FROM N.A.  
RA TISSUE=Placenta;  
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagaetsuma M., Hoshino T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi S., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Yamamoto K., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto K., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,  
RA Nishimura K., Iwayanagi T.;  
RT "NEO human cDNA sequencing project.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]

RP REVIEW.  
 RX MEDLINE=21474438; PubMed=11590207;  
 RA Schmitz G., Langmann T., Heimert S.;  
 RT "Role of ABCG1 and other ABCG family members in lipid metabolism.";   
 RL J. Lipid Res. 42:1513-1520(2001).  
 CC -1- FUNCTION: XENOBIOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE  
 CC IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST  
 CC CANCER CELL LINE. WHEN OVEREXPRESSED, THE TRANSECTED CELLS BECOME  
 CC RESISTANT TO MITOANTHRONE, DAUNORUBICIN AND DOXORUBICIN, DISPLAY  
 CC DIMINISHED INTRACELLULAR ACCUMULATION OF DAUNORUBICIN, AND  
 CC MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)  
 CC SUBFAMILY.  
 -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>  
 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 -----  
 CC EMBL, AF103796; AAD09188.1; -;  
 DR EMBL, AF098951; AAC97367.1; -;  
 DR EMBL, AB056867; BAB39212.1; -;  
 DR EMBL, AK002040; BAA92050.1; -;  
 DR Genew, HGNC:74; ABCG2.  
 DR MIM, 603756; -;  
 DR GO, GO:0016021; C:integral to membrane; TAS.  
 DR GO, GO:0005524; F:ATP binding activity; TAS.  
 DR GO, GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; TAS.  
 DR GO, GO:0005215; F:transporter activity; TAS.  
 DR GO, GO:0005559; F:xenobiotic-transporting ATPase activity; TAS.  
 DR GO, GO:000315; P:drug resistance; TAS.  
 DR GO, GO:0006832; P:small molecule transport; TAS.  
 DR InterPro, IPR003593; AAA\_ATPase.  
 DR InterPro, IPR003439; ABC\_transporter.  
 DR Pfam, PF00005; ABC\_tran; 1.  
 DR ProDom, PD000006; ABC\_transporter; 1.  
 DR SMART, SM00382; AAA; 1.  
 DR PROSITE, PS00211; ABC\_TRANSPORTER\_1; FALSE\_NEG.  
 DR PROSITE, PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Transmembrane; Transport.  
 FT DOMAIN 1 395  
 FT TRANSMEM 396 416  
 FT DOMAIN 417 428  
 FT TRANSMEM 429 449  
 FT DOMAIN 450 477  
 FT TRANSMEM 478 498  
 FT TRANSMEM 499 506  
 FT TRANSMEM 507 527  
 FT TRANSMEM 528 535  
 FT TRANSMEM 536 556  
 FT TRANSMEM 557 630  
 FT TRANSMEM 631 651  
 FT DOMAIN 652 655  
 FT NP BIND 80 87  
 FT CARBOHYD 418 418  
 FT CARBOHYD 557 557  
 FT CARBOHYD 556 556  
 FT CONFLICT 24 24  
 FT CONFLICT 166 166  
 FT CONFLICT 208 208  
 FT CONFLICT 315 315  
 FT CONFLICT 482 482  
 FT CONFLICT 482 482  
 FT SEQUENCE 655 AA; 72343 MW; 89A6D511DC5C60 CRC64;  
 Query Match 99.8%; Score 3344; DB 1; Length 655;  
 Best Local Similarity 99.8%; Pred. No. 3.3e-221;  
 Matches 654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MSSSVBVFIPVSGNTNGPFAIVSNDLKAFTGAVLSFPHNICRVKLSGFLPKRQVE 60  
 QY KEILSINIGIMKPGALNALTGTGGKSSLDVLAARPDPSGLSDVLINGAPRANFKCN 120  
 DB 61 KEILSINIGIMKPGALNALTGTGGKSSLDVLAARPDPSGLSDVLINGAPRANFKCN 120  
 QY SGYVQDDVWVWGLTLVRNLOPSAALRLATTMTNHEKERNINRYEELGLDKVADSKGT 180  
 DB 121 SGYVQDDVWVWGLTLVRNLOPSAALRLATTMTNHEKERNINRYEELGLDKVADSKGT 180  
 QY SGYVQDDVWVWGLTLVRNLOPSAALRLATTMTNHEKERNINRYEELGLDKVADSKGT 180  
 DB 121 SGYVQDDVWVWGLTLVRNLOPSAALRLATTMTNHEKERNINRYEELGLDKVADSKGT 180  
 QY OPIRGVSGEKKRTSIGMELITDPSILSLDEPTTGLDSTANAVLLKRSKQORTIIF 240  
 DB 181 OPIRGVSGEKKRTSIGMELITDPSILSLDEPTTGLDSTANAVLLKRSKQORTIIF 240  
 QY OPIRGVSGEKKRTSIGMELITDPSILSLDEPTTGLDSTANAVLLKRSKQORTIIF 240  
 DB 181 OPIRGVSGEKKRTSIGMELITDPSILSLDEPTTGLDSTANAVLLKRSKQORTIIF 240  
 QY SIHOPRYSIFPLPSLTLLASGRMLFHPGPAQALGYFESAGYHCEAYNNPADFLDIING 300  
 DB 241 SIHOPRYSIFPLPSLTLLASGRMLFHPGPAQALGYFESAGYHCEAYNNPADFLDIING 300  
 QY SIHOPRYSIFPLPSLTLLASGRMLFHPGPAQALGYFESAGYHCEAYNNPADFLDIING 300  
 DB 241 SIHOPRYSIFPLPSLTLLASGRMLFHPGPAQALGYFESAGYHCEAYNNPADFLDIING 300  
 QY DSTAVALNREDFPKATEIIEPSKODKPLIEKLAETIYNSSTYKGTAKELHOLSGEKKK 360  
 DB 301 DSTAVALNREDFPKATEIIEPSKODKPLIEKLAETIYNSSTYKGTAKELHOLSGEKKK 360  
 QY DSTAVALNREDFPKATEIIEPSKODKPLIEKLAETIYNSSTYKGTAKELHOLSGEKKK 360  
 DB 301 DSTAVALNREDFPKATEIIEPSKODKPLIEKLAETIYNSSTYKGTAKELHOLSGEKKK 360  
 QY ITVFKEISYTSFCHOLRWVSKSPKULGNPOASIAQIYTVVLGLVIGAIYFGLKXDS 420  
 DB 361 ITVFKEISYTSFCHOLRWVSKSPKULGNPOASIAQIYTVVLGLVIGAIYFGLKXDS 420  
 QY ITVFKEISYTSFCHOLRWVSKSPKULGNPOASIAQIYTVVLGLVIGAIYFGLKXDS 420  
 DB 361 ITVFKEISYTSFCHOLRWVSKSPKULGNPOASIAQIYTVVLGLVIGAIYFGLKXDS 420  
 QY TGIONRAGVLFPLTNGCFSSVSAVELFVVEKKLFIHEIYISGYRVSSYFGLKLSDLPL 480  
 DB 421 TGIONRAGVLFPLTNGCFSSVSAVELFVVEKKLFIHEIYISGYRVSSYFGLKLSDLPL 480  
 QY TGIONRAGVLFPLTNGCFSSVSAVELFVVEKKLFIHEIYISGYRVSSYFGLKLSDLPL 480  
 DB 421 TGIONRAGVLFPLTNGCFSSVSAVELFVVEKKLFIHEIYISGYRVSSYFGLKLSDLPL 480  
 QY MRMLPSIIFTCIYVFMGLKPKADAFYVMFTLMWAVASASSMALAIAGOSVVSATLL 540  
 DB 481 MRMLPSIIFTCIYVFMGLKPKADAFYVMFTLMWAVASASSMALAIAGOSVVSATLL 540  
 QY MRMLPSIIFTCIYVFMGLKPKADAFYVMFTLMWAVASASSMALAIAGOSVVSATLL 540  
 DB 481 MRMLPSIIFTCIYVFMGLKPKADAFYVMFTLMWAVASASSMALAIAGOSVVSATLL 540  
 QY MTICVFPMISGGLVNLTTASWLSWLOYSIRYGTALQNHPEFGQNCPCGNATGN 600  
 DB 541 MTICVFPMISGGLVNLTTASWLSWLOYSIRYGTALQNHPEFGQNCPCGNATGN 600  
 QY MTICVFPMISGGLVNLTTASWLSWLOYSIRYGTALQNHPEFGQNCPCGNATGN 600  
 DB 541 MTICVFPMISGGLVNLTTASWLSWLOYSIRYGTALQNHPEFGQNCPCGNATGN 600  
 QY NPCVATCTGGRYLVKQIDLSPMGLMKNHVALACMIVIFLTIYVLLFLPKKYS 655  
 DB 601 NPCVATCTGGRYLVKQIDLSPMGLMKNHVALACMIVIFLTIYVLLFLPKKYS 655  
 QY NPCVATCTGGRYLVKQIDLSPMGLMKNHVALACMIVIFLTIYVLLFLPKKYS 655  
 DB 601 NPCVATCTGGRYLVKQIDLSPMGLMKNHVALACMIVIFLTIYVLLFLPKKYS 655

RESULT 2  
 ABG3\_MOUSE  
 ID ABG3\_MOUSE STANDARD; PRT: 650 AA.  
 AC 099P81.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ATP-binding cassette, sub-family G, member 3.  
 GN ABCG3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 OX (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=21030753; PubMed=11178751;  
 RA Micklethwait L., Jain P., Miyake K., Schriml L.M., Rao K., Fojo T.,  
 RA Bates S., Dean M.;  
 RT "An ATP-binding cassette gene (ABCG3) closely related to the multidrug  
 RT transporter ABCG2 (MXR/ABCP) has an unusual ATP-binding domain.";  
 RL Mamm Genome 12:86-88(2001).  
 CC -1- SUBUNIT: May dimerize with another subunit to form a functional  
 CC transporter.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- TISSUE SPECIFICITY: Highest levels of expression in thymus and  
 CC spleen. Detected in lung and small intestine.  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)  
 CC SUBFAMILY.

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2003, 18:38:41 ; Search time 5.49875 Seconds  
(without alignments)  
1257.181 Million cell updates/sec

Title: US-09-856-927-4

Perfect score: 769  
Sequence: 1 FELGAEVYASSMALAIATG.....MIIFETIAYKLFLPKKYS 147

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623	81.0	655	1	ABG2_HUMAN
2	414.5	53.9	650	1	ABG2_MOUSE
3	128	16.6	687	1	WHIT_DROME
4	124.5	16.2	1499	1	CDR2_CANAL
5	123.5	16.1	646	1	ABG4_HUMAN
6	113	14.7	678	1	ABG1_HUMAN
7	110.5	14.4	1333	1	YN99_YEAST
8	110	14.3	666	1	ABG1_MOUSE
9	109.5	14.2	1501	1	CDR1_CANAL
10	109.5	14.1	598	1	YPC3_CAEEL
11	108.5	14.0	1294	1	YH5S_YEAST
12	108	13.7	679	1	WHIT_CERCA
13	105	13.3	1564	1	PDRB_YEAST
14	102.5	12.9	1410	1	PDRB_YEAST
15	99.5	12.3	610	1	YOSC_CAEEL
16	97	12.6	1501	1	CDR3_CANAL
17	94.5	12.3	601	1	YOSC_CAEEL
18	94.5	12.3	677	1	WHIT_LUCCU
19	91.5	11.9	1530	1	BPR1_GCHPO
20	87	11.3	1529	1	PDRF_YEAST
21	86	11.2	1490	1	CDR4_CANAL
22	85	11.1	695	1	WHIT_ANOGA
23	83.5	10.9	1511	1	PDR5_YEAST
24	82.5	10.7	651	1	ABG5_HUMAN
25	81.5	10.6	652	1	ABG5_MOUSE
26	81.5	10.5	1511	1	PDR5_YEAST
27	81	10.5	672	1	ABG8_YEAST
28	80	10.4	661	1	BIO5_YEAST
29	79.5	10.3	275	1	YD84_YEAST
30	79	10.3	839	1	NAH3_OIDMA
31	78.5	10.2	709	1	WHIT_ANOAL
32	78.5	10.2	709	1	WHIT_ANOAL
33	76.5	9.9	364	1	YH1M_ECOLI

34	76.5	9.9	652	1	ABG5_RAT	Q99pe7 ratius nov
35	76.5	9.9	656	1	YID7_YEAST	P40534 saccharomyc
36	75.5	9.8	518	1	SPK5_BACSU	P000758 bacillus su
37	74.5	9.7	142	1	YNK5_YEAST	P50943 saccharomyc
38	74.5	9.7	1049	1	ADP1_YEAST	P25371 saccharomyc
39	74	9.6	149	1	DISD_DICDI	P02887 dictyostell
40	74	9.6	253	1	YF1G_BACSU	P54723 bacillus su
41	74	9.6	831	1	NAH3_RAT	P26433 ratius nov
42	73	9.5	527	1	COX1_YEAST	O07063 arabidopsis
43	73	9.5	590	1	ABG8_YEAST	P04817 saccharomyc
44	73	9.5	673	1	ABG8_MOUSE	Q9dbm0 mus musculu
45	73	9.5	673	1	ABG8_MOUSE	Q9dbm0 mus musculu

## ALIGNMENTS

RESULT 1  
ABG2\_HUMAN  
ID ABG2\_HUMAN STANDARD; PRT; 655 AA.  
AC Q9UNQ0; Q95374; Q9BY73; Q9NUS0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE ATP-binding cassette, sub-family G, member 2 (placenta-specific ATP-binding cassette transporter) (Breast cancer resistance protein).  
DE ABCG2 OR ABCP OR BCRP OR BCRP1.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
OX [1]  
RN [1]  
RC TISSUE=Placenta;  
RX MEDLINE=99065313; PubMed=9850061;  
RA Allikmets R., Schriml L.M., Hutchinson A., Romano-Spica V., Dean M.;  
RT "A human placenta-specific ATP-binding cassette gene (ABCP) on chromosome 4q22 that is involved in multidrug resistance.";  
RL Cancer Res. 58:5337-5339(1998).  
RN [2]  
RN [3]  
RA "Breast cancer resistance protein transporter from human MCF-7 breast cancer cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:15665-15670(1998).  
RN [4]  
RA "Breast cancer resistance protein transporter from human MCF-7 breast cancer cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:2569-2569(1999).  
RN [5]  
RA "Breast cancer resistance protein transporter from human MCF-7 breast cancer cells.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RA "Breast cancer resistance protein transporter from human MCF-7 breast cancer cells.";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RP REVIEW.  
 RX MEDLINE=21474438; PubMed=11590207;  
 RA Schmitz G., Langmann T., Helmerl S.;  
 RT Role of ABCG1 and other ABCG family members in lipid metabolism.";  
 RL J. Lipid Res. 42:1513-1520(2001).  
 CC -1- FUNCTION: XENOBIOTIC TRANSPORTER THAT APPEARS TO PLAY A MAJOR ROLE  
 CC IN THE MULTIDRUG RESISTANCE PHENOTYPE OF A SPECIFIC MCF-7 BREAST  
 CC CANCER CELL LINE. WHEN OVEREXPRESSED, THE TRANSECTED CELLS BECOME  
 CC RESISTANT TO MITOXANTHONE, DAUNORUBICIN AND DOXORUBICIN, DISPLAY  
 CC DIMINISHED INTRACELLULAR ACCUMULATION OF DAUNORUBICIN, AND  
 CC MANIFEST AN ATP-DEPENDENT INCREASE IN THE EFFLUX OF RHODAMINE 123.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCG (WHITE)  
 CC SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL/ AF103796; AAD09188.1; -;  
 DR EMBL/ AP098851; AAC97367.1; -;  
 DR EMBL/ AB056867; BAB39212.1; -;  
 DR EMBL/ AK002040; BAA92050.1; -;  
 DR Genew; HGNC:74; ABCG2.  
 DR MIM; 603756; -;  
 DR GO; GO:0016021; C: integral to membrane; TAS.  
 DR GO; GO:0005524; F: ATP binding activity; TAS.  
 DR GO; GO:0004009; F: ATP-binding cassette (ABC) transporter acti. . .; TAS.  
 DR GO; GO:0008515; F: xenobiotic activity; TAS.  
 DR GO; GO:0008515; F: xenobiotic-transporting ATPase activity; TAS.  
 DR GO; GO:0006832; P: drug resistance; TAS.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SMO00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; FALSE\_NEG.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KM ATP-binding; Transmembrane; Transport.  
 FT DOMAIN 1 395  
 FT TRANSMEM 396 416  
 FT TRANSMEM 417 428  
 FT TRANSMEM 429 449  
 FT DOMAIN 450 477  
 FT TRANSMEM 478 498  
 FT TRANSMEM 499 506  
 FT TRANSMEM 507 527  
 FT TRANSMEM 528 535  
 FT TRANSMEM 536 556  
 FT TRANSMEM 557 630  
 FT TRANSMEM 631 651  
 FT TRANSMEM 652 655  
 FT DOMAIN 656 87  
 FT NE\_BIND 80 87  
 FT CARBOHYD 418 418  
 FT CARBOHYD 557 557  
 FT CARBOHYD 558 558  
 FT CARBOHYD 559 559  
 FT CARBOHYD 560 560  
 FT CARBOHYD 561 561  
 FT CARBOHYD 562 562  
 FT CARBOHYD 563 563  
 FT CARBOHYD 564 564  
 FT CARBOHYD 565 565  
 FT CARBOHYD 566 566  
 FT CARBOHYD 567 567  
 FT CARBOHYD 568 568  
 FT CARBOHYD 569 569  
 FT CARBOHYD 570 570  
 FT CARBOHYD 571 571  
 FT CARBOHYD 572 572  
 FT CARBOHYD 573 573  
 FT CARBOHYD 574 574  
 FT CARBOHYD 575 575  
 FT CARBOHYD 576 576  
 FT CARBOHYD 577 577  
 FT CARBOHYD 578 578  
 FT CARBOHYD 579 579  
 FT CARBOHYD 580 580  
 FT CARBOHYD 581 581  
 FT CARBOHYD 582 582  
 FT CARBOHYD 583 583  
 FT CARBOHYD 584 584  
 FT CARBOHYD 585 585  
 FT CARBOHYD 586 586  
 FT CARBOHYD 587 587  
 FT CARBOHYD 588 588  
 FT CARBOHYD 589 589  
 FT CARBOHYD 590 590  
 FT CARBOHYD 591 591  
 FT CARBOHYD 592 592  
 FT CARBOHYD 593 593  
 FT CARBOHYD 594 594  
 FT CARBOHYD 595 595  
 FT CARBOHYD 596 596  
 FT CARBOHYD 597 597  
 FT CARBOHYD 598 598  
 FT CARBOHYD 599 599  
 FT CARBOHYD 600 600  
 FT CARBOHYD 601 601  
 FT CARBOHYD 602 602  
 FT CARBOHYD 603 603  
 FT CARBOHYD 604 604  
 FT CARBOHYD 605 605  
 FT CARBOHYD 606 606  
 FT CARBOHYD 607 607  
 FT CARBOHYD 608 608  
 FT CARBOHYD 609 609  
 FT CARBOHYD 610 610  
 FT CARBOHYD 611 611  
 FT CARBOHYD 612 612  
 FT CARBOHYD 613 613  
 FT CARBOHYD 614 614  
 FT CARBOHYD 615 615  
 FT CARBOHYD 616 616  
 FT CARBOHYD 617 617  
 FT CARBOHYD 618 618  
 FT CARBOHYD 619 619  
 FT CARBOHYD 620 620  
 FT CARBOHYD 621 621  
 FT CARBOHYD 622 622  
 FT CARBOHYD 623 623  
 FT CARBOHYD 624 624  
 FT CARBOHYD 625 625  
 FT CARBOHYD 626 626  
 FT CARBOHYD 627 627  
 FT CARBOHYD 628 628  
 FT CARBOHYD 629 629  
 FT CARBOHYD 630 630  
 FT CARBOHYD 631 631  
 FT CARBOHYD 632 632  
 FT CARBOHYD 633 633  
 FT CARBOHYD 634 634  
 FT CARBOHYD 635 635  
 FT CARBOHYD 636 636  
 FT CARBOHYD 637 637  
 FT CARBOHYD 638 638  
 FT CARBOHYD 639 639  
 FT CARBOHYD 640 640  
 FT CARBOHYD 641 641  
 FT CARBOHYD 642 642  
 FT CARBOHYD 643 643  
 FT CARBOHYD 644 644  
 FT CARBOHYD 645 645  
 FT CARBOHYD 646 646  
 FT CARBOHYD 647 647  
 FT CARBOHYD 648 648  
 FT CARBOHYD 649 649  
 FT CARBOHYD 650 650  
 FT CARBOHYD 651 651  
 FT CARBOHYD 652 652  
 FT CARBOHYD 653 653  
 FT CARBOHYD 654 654  
 FT CARBOHYD 655 655  
 FT CARBOHYD 656 656  
 FT CARBOHYD 657 657  
 FT CARBOHYD 658 658  
 FT CARBOHYD 659 659  
 FT CARBOHYD 660 660  
 FT CARBOHYD 661 661  
 FT CARBOHYD 662 662  
 FT CARBOHYD 663 663  
 FT CARBOHYD 664 664  
 FT CARBOHYD 665 665  
 FT CARBOHYD 666 666  
 FT CARBOHYD 667 667  
 FT CARBOHYD 668 668  
 FT CARBOHYD 669 669  
 FT CARBOHYD 670 670  
 FT CARBOHYD 671 671  
 FT CARBOHYD 672 672  
 FT CARBOHYD 673 673  
 FT CARBOHYD 674 674  
 FT CARBOHYD 675 675  
 FT CARBOHYD 676 676  
 FT CARBOHYD 677 677  
 FT CARBOHYD 678 678  
 FT CARBOHYD 679 679  
 FT CARBOHYD 680 680  
 FT CARBOHYD 681 681  
 FT CARBOHYD 682 682  
 FT CARBOHYD 683 683  
 FT CARBOHYD 684 684  
 FT CARBOHYD 685 685  
 FT CARBOHYD 686 686  
 FT CARBOHYD 687 687  
 FT CARBOHYD 688 688  
 FT CARBOHYD 689 689  
 FT CARBOHYD 690 690  
 FT CARBOHYD 691 691  
 FT CARBOHYD 692 692  
 FT CARBOHYD 693 693  
 FT CARBOHYD 694 694  
 FT CARBOHYD 695 695  
 FT CARBOHYD 696 696  
 FT CARBOHYD 697 697  
 FT CARBOHYD 698 698  
 FT CARBOHYD 699 699  
 FT CARBOHYD 700 700  
 FT CARBOHYD 701 701  
 FT CARBOHYD 702 702  
 FT CARBOHYD 703 703  
 FT CARBOHYD 704 704  
 FT CARBOHYD 705 705  
 FT CARBOHYD 706 706  
 FT CARBOHYD 707 707  
 FT CARBOHYD 708 708  
 FT CARBOHYD 709 709  
 FT CARBOHYD 710 710  
 FT CARBOHYD 711 711  
 FT CARBOHYD 712 712  
 FT CARBOHYD 713 713  
 FT CARBOHYD 714 714  
 FT CARBOHYD 715 715  
 FT CARBOHYD 716 716  
 FT CARBOHYD 717 717  
 FT CARBOHYD 718 718  
 FT CARBOHYD 719 719  
 FT CARBOHYD 720 720  
 FT CARBOHYD 721 721  
 FT CARBOHYD 722 722  
 FT CARBOHYD 723 723  
 FT CARBOHYD 724 724  
 FT CARBOHYD 725 725  
 FT CARBOHYD 726 726  
 FT CARBOHYD 727 727  
 FT CARBOHYD 728 728  
 FT CARBOHYD 729 729  
 FT CARBOHYD 730 730  
 FT CARBOHYD 731 731  
 FT CARBOHYD 732 732  
 FT CARBOHYD 733 733  
 FT CARBOHYD 734 734  
 FT CARBOHYD 735 735  
 FT CARBOHYD 736 736  
 FT CARBOHYD 737 737  
 FT CARBOHYD 738 738  
 FT CARBOHYD 739 739  
 FT CARBOHYD 740 740  
 FT CARBOHYD 741 741  
 FT CARBOHYD 742 742  
 FT CARBOHYD 743 743  
 FT CARBOHYD 744 744  
 FT CARBOHYD 745 745  
 FT CARBOHYD 746 746  
 FT CARBOHYD 747 747  
 FT CARBOHYD 748 748  
 FT CARBOHYD 749 749  
 FT CARBOHYD 750 750  
 FT CARBOHYD 751 751  
 FT CARBOHYD 752 752  
 FT CARBOHYD 753 753  
 FT CARBOHYD 754 754  
 FT CARBOHYD 755 755  
 FT CARBOHYD 756 756  
 FT CARBOHYD 757 757  
 FT CARBOHYD 758 758  
 FT CARBOHYD 759 759  
 FT CARBOHYD 760 760  
 FT CARBOHYD 761 761  
 FT CARBOHYD 762 762  
 FT CARBOHYD 763 763  
 FT CARBOHYD 764 764  
 FT CARBOHYD 765 765  
 FT CARBOHYD 766 766  
 FT CARBOHYD 767 767  
 FT CARBOHYD 768 768  
 FT CARBOHYD 769 769  
 FT CARBOHYD 770 770  
 FT CARBOHYD 771 771  
 FT CARBOHYD 772 772  
 FT CARBOHYD 773 773  
 FT CARBOHYD 774 774  
 FT CARBOHYD 775 775  
 FT CARBOHYD 776 776  
 FT CARBOHYD 777 777  
 FT CARBOHYD 778 778  
 FT CARBOHYD 779 779  
 FT CARBOHYD 780 780  
 FT CARBOHYD 781 781  
 FT CARBOHYD 782 782  
 FT CARBOHYD 783 783  
 FT CARBOHYD 784 784  
 FT CARBOHYD 785 785  
 FT CARBOHYD 786 786  
 FT CARBOHYD 787 787  
 FT CARBOHYD 788 788  
 FT CARBOHYD 789 789  
 FT CARBOHYD 790 790  
 FT CARBOHYD 791 791  
 FT CARBOHYD 792 792  
 FT CARBOHYD 793 793  
 FT CARBOHYD 794 794  
 FT CARBOHYD 795 795  
 FT CARBOHYD 796 796  
 FT CARBOHYD 797 797  
 FT CARBOHYD 798 798  
 FT CARBOHYD 799 799  
 FT CARBOHYD 800 800  
 FT CARBOHYD 801 801  
 FT CARBOHYD 802 802  
 FT CARBOHYD 803 803  
 FT CARBOHYD 804 804  
 FT CARBOHYD 805 805  
 FT CARBOHYD 806 806  
 FT CARBOHYD 807 807  
 FT CARBOHYD 808 808  
 FT CARBOHYD 809 809  
 FT CARBOHYD 810 810  
 FT CARBOHYD 811 811  
 FT CARBOHYD 812 812  
 FT CARBOHYD 813 813  
 FT CARBOHYD 814 814  
 FT CARBOHYD 815 815  
 FT CARBOHYD 816 816  
 FT CARBOHYD 817 817  
 FT CARBOHYD 818 818  
 FT CARBOHYD 819 819  
 FT CARBOHYD 820 820  
 FT CARBOHYD 821 821  
 FT CARBOHYD 822 822  
 FT CARBOHYD 823 823  
 FT CARBOHYD 824 824  
 FT CARBOHYD 825 825  
 FT CARBOHYD 826 826  
 FT CARBOHYD 827 827  
 FT CARBOHYD 828 828  
 FT CARBOHYD 829 829  
 FT CARBOHYD 830 830  
 FT CARBOHYD 831 831  
 FT CARBOHYD 832 832  
 FT CARBOHYD 833 833  
 FT CARBOHYD 834 834  
 FT CARBOHYD 835 835  
 FT CARBOHYD 836 836  
 FT CARBOHYD 837 837  
 FT CARBOHYD 838 838  
 FT CARBOHYD 839 839  
 FT CARBOHYD 840 840  
 FT CARBOHYD 841 841  
 FT CARBOHYD 842 842  
 FT CARBOHYD 843 843  
 FT CARBOHYD 844 844  
 FT CARBOHYD 845 845  
 FT CARBOHYD 846 846  
 FT CARBOHYD 847 847  
 FT CARBOHYD 848 848  
 FT CARBOHYD 849 849  
 FT CARBOHYD 850 850  
 FT CARBOHYD 851 851  
 FT CARBOHYD 852 852  
 FT CARBOHYD 853 853  
 FT CARBOHYD 854 854  
 FT CARBOHYD 855 855  
 FT CARBOHYD 856 856  
 FT CARBOHYD 857 857  
 FT CARBOHYD 858 858  
 FT CARBOHYD 859 859  
 FT CARBOHYD 860 860  
 FT CARBOHYD 861 861  
 FT CARBOHYD 862 862  
 FT CARBOHYD 863 863  
 FT CARBOHYD 864 864  
 FT CARBOHYD 865 865  
 FT CARBOHYD 866 866  
 FT CARBOHYD 867 867  
 FT CARBOHYD 868 868  
 FT CARBOHYD 869 869  
 FT CARBOHYD 870 870  
 FT CARBOHYD 871 871  
 FT CARBOHYD 872 872  
 FT CARBOHYD 873 873  
 FT CARBOHYD 874 874  
 FT CARBOHYD 875 875  
 FT CARBOHYD 876 876  
 FT CARBOHYD 877 877  
 FT CARBOHYD 878 878  
 FT CARBOHYD 879 879  
 FT CARBOHYD 880 880  
 FT CARBOHYD 881 881  
 FT CARBOHYD 882 882  
 FT CARBOHYD 883 883  
 FT CARBOHYD 884 884  
 FT CARBOHYD 885 885  
 FT CARBOHYD 886 886  
 FT CARBOHYD 887 887  
 FT CARBOHYD 888 888  
 FT CARBOHYD 889 889  
 FT CARBOHYD 890 890  
 FT CARBOHYD 891 891  
 FT CARBOHYD 892 892  
 FT CARBOHYD 893 893  
 FT CARBOHYD 894 894  
 FT CARBOHYD 895 895  
 FT CARBOHYD 896 896  
 FT CARBOHYD 897 897  
 FT CARBOHYD 898 898  
 FT CARBOHYD 899 899  
 FT CARBOHYD 900 900  
 FT CARBOHYD 901 901  
 FT CARBOHYD 902 902  
 FT CARBOHYD 903 903  
 FT CARBOHYD 904 904  
 FT CARBOHYD 905 905  
 FT CARBOHYD 906 906  
 FT CARBOHYD 907 907  
 FT CARBOHYD 908 908  
 FT CARBOHYD 909 909  
 FT CARBOHYD 910 910  
 FT CARBOHYD 911 911  
 FT CARBOHYD 912 912  
 FT CARBOHYD 913 913  
 FT CARBOHYD 914 914  
 FT CARBOHYD 915 915  
 FT CARBOHYD 916 916  
 FT CARBOHYD 917 917  
 FT CARBOHYD 918 918  
 FT CARBOHYD 919 919  
 FT CARBOHYD 920 920  
 FT CARBOHYD 921 921  
 FT CARBOHYD 922 922  
 FT CARBOHYD 923 923  
 FT CARBOHYD 924 924  
 FT CARBOHYD 925 925  
 FT CARBOHYD 926 926  
 FT CARBOHYD 927 927  
 FT CARBOHYD 928 928  
 FT CARBOHYD 929 929  
 FT CARBOHYD 930 930  
 FT CARBOHYD 931 931  
 FT CARBOHYD 932 932  
 FT CARBOHYD 933 933  
 FT CARBOHYD 934 934  
 FT CARBOHYD 935 935  
 FT CARBOHYD 936 936  
 FT CARBOHYD 937 937  
 FT CARBOHYD 938 938  
 FT CARBOHYD 939 939  
 FT CARBOHYD 940 940  
 FT CARBOHYD 941 941  
 FT CARBOHYD 942 942  
 FT CARBOHYD 943 943  
 FT CARBOHYD 944 944  
 FT CARBOHYD 945 945  
 FT CARBOHYD 946 946  
 FT CARBOHYD 947 947  
 FT CARBOHYD 948 948  
 FT CARBOHYD 949 949  
 FT CARBOHYD 950 950  
 FT CARBOHYD 951 951  
 FT CARBOHYD 952 952  
 FT CARBOHYD 953 953  
 FT CARBOHYD 954 954  
 FT CARBOHYD 955 955  
 FT CARBOHYD 956 956  
 FT CARBOHYD 957 957  
 FT CARBOHYD 958 958  
 FT CARBOHYD 959 959  
 FT CARBOHYD 960 960  
 FT CARBOHYD 961 961  
 FT CARBOHYD 962 962  
 FT CARBOHYD 963 963  
 FT CARBOHYD 964 964  
 FT CARBOHYD 965 965  
 FT CARBOHYD 966 966  
 FT CARBOHYD 967 967  
 FT CARBOHYD 968 968  
 FT CARBOHYD 969 969  
 FT CARBOHYD 970 970  
 FT CARBOHYD 971 971  
 FT CARBOHYD 972 972  
 FT CARBOHYD 973 973  
 FT CARBOHYD 974 974  
 FT CARBOHYD 975 975  
 FT CARBOHYD 976 976  
 FT CARBOHYD 977 977  
 FT CARBOHYD 978 978  
 FT CARBOHYD 979 979  
 FT CARBOHYD 980 980  
 FT CARBOHYD 981 981  
 FT CARBOHYD 982 982  
 FT CARBOHYD 983 983  
 FT CARBOHYD 984 984  
 FT CARBOHYD 985 985  
 FT CARBOHYD 986 986  
 FT CARBOHYD 987 987  
 FT CARBOHYD 988 988  
 FT CARBOHYD 989 989  
 FT CARBOHYD 990 990  
 FT CARBOHYD 991 991  
 FT CARBOHYD 992 992  
 FT CARBOHYD 993 993  
 FT CARBOHYD 994 994  
 FT CARBOHYD 995 995  
 FT CARBOHYD 996 996  
 FT CARBOHYD 997 997  
 FT CARBOHYD 998 998  
 FT CARBOHYD 999 999  
 FT CARBOHYD 1000 1000  
 FT CARBOHYD 1001 1001  
 FT CARBOHYD 1002 1002  
 FT CARBOHYD 1003 1003  
 FT CARBOHYD 1004 1004  
 FT CARBOHYD 1005 1005  
 FT CARBOHYD 1006 1006  
 FT CARBOHYD 1007 1007  
 FT CARBOHYD 1008 1008  
 FT CARBOHYD 1009 1009  
 FT CARBOHYD 1010 1010  
 FT CARBOHYD 1011 1011  
 FT CARBOHYD 1012 1012  
 FT CARBOHYD 1013 1013  
 FT CARBOHYD 1014 1014  
 FT CARBOHYD 1015 1015  
 FT CARBOHYD 1016 1016  
 FT CARBOHYD 1017 1017  
 FT CARBOHYD 1018 1018  
 FT CARBOHYD 1019 1019  
 FT CARBOHYD 1020 1020  
 FT CARBOHYD 1021 1021  
 FT CARBOHYD 1022 1022  
 FT CARBOHYD 1023 1023  
 FT CARBOHYD 1024 1024  
 FT CARBOHYD 1025 1025  
 FT CARBOHYD 1026 1026  
 FT CARBOHYD 1027 1027  
 FT CARBOHYD 1028 1028  
 FT CARBOHYD 1029 1029  
 FT CARBOHYD 1030 1030  
 FT CARBOHYD 1031 1031  
 FT CARBOHYD 1032 1032  
 FT CARBOHYD 1033 1033  
 FT CARBOHYD 1034 1034  
 FT CARBOHYD 1035 1035  
 FT CARBOHYD 1036 1036  
 FT CARBOHYD 1037 1037  
 FT CARBOHYD 1038 1038  
 FT CARBOHYD 1039 1039  
 FT CARBOHYD 1040 1040  
 FT CARBOHYD 1041 1041  
 FT CARBOHYD 1042 1042  
 FT CARBOHYD 1043 1043  
 FT CARBOHYD 1044 1044  
 FT CARBOHYD 1045 1045  
 FT CARBOHYD 1046 1046  
 FT CARBOHYD 1047 1047  
 FT CARBOHYD 1048 1048  
 FT CARBOHYD 1049 1049  
 FT CARBOHYD 1050 1050  
 FT CARBOHYD 1051 1051  
 FT CARBOHYD 1052 1052  
 FT CARBOHYD 1053 1053  
 FT CARBOHYD 1054 1054  
 FT CARBOHYD 1055 1055  
 FT CARBOHYD 1056 1056  
 FT CARBOHYD 1057 1057  
 FT CARBOHYD 1058 1058  
 FT CARBOHYD 1059 1059  
 FT CARBOHYD 1060 1060  
 FT CARBOHYD 1061 1061  
 FT CARBOHYD 1062 1062  
 FT CARBOHYD 1063 1063  
 FT CARBOHYD 1064 1064  
 FT CARBOHYD 1065 1065  
 FT CARBOHYD 1066 1066  
 FT CARBOHYD 1067 1067  
 FT CARBOHYD 1068 1068  
 FT CARBOHYD 1069 1069  
 FT CARBOHYD 1070 1070  
 FT CARBOHYD 1071 1071  
 FT CARBOHYD 1072 1072  
 FT CARBOHYD 1073 1073  
 FT CARBOHYD 1074 1074  
 FT CARBOHYD 1075 1075  
 FT CARBOHYD 1076 1076  
 FT CARBOHYD 1077 1077  
 FT CARBOHYD 1078 1078  
 FT CARBOHYD 1079 1079  
 FT CARBOHYD 1080 1080  
 FT CARBOHYD 1081 1081  
 FT CARBOHYD 1082 1082  
 FT CARBOHYD 1083 1083  
 FT CARBOHYD 1084 1084  
 FT CARBOHYD 1085 1085  
 FT CARBOHYD 1086 1086  
 FT CARBOHYD 1087 1087  
 FT CARBOHYD 1088 1088  
 FT CARBOHYD 1089 1089  
 FT CARBOHYD 1090 1090  
 FT CARBOHYD 1091 1091  
 FT CARBOHYD 1092 1092  
 FT CARBOHYD 1093 1093  
 FT CARBOHYD 1094 1094  
 FT CARBOHYD 1095 1095  
 FT CARBOHYD 1096 1096  
 FT CARBOHYD 1097 1097  
 FT CARBOHYD 1098 1098  
 FT CARBOHYD 1099 1099  
 FT CARBOHYD 1100 1100  
 FT CARBOHYD 1101 1101  
 FT CARBOHYD 1102 1102  
 FT CARBOHYD 1103 1103  
 FT CARBOHYD 1104 1104  
 FT CARBOHYD 1105 1105  
 FT CARBOHYD 1106 1106  
 FT CARBOHYD 1107 1107  
 FT CARBOHYD 1108 1108  
 FT CARBOHYD 1109 1109  
 FT CARBOHYD 1110 1110  
 FT CARBOHYD 1111 1111  
 FT CARBOHYD 1112 1112  
 FT CARBOHYD 1113 1113  
 FT CARBOHYD 1114 1114  
 FT CARBOHYD 1115 1115  
 FT CARBOHYD 1116 1116  
 FT CARBOHYD 1117 1117  
 FT CARBOHYD 1118 1118  
 FT CARBOHYD 1119 1119  
 FT CARBOHYD 1120 1120  
 FT CARBOHYD 1121 1121  
 FT CARBOHYD 1122 1122  
 FT CARBOHYD 1123 1123  
 FT CARBOHYD 1124 1124  
 FT CARBOHYD 1125 1125  
 FT CARBOHYD 1126 1126  
 FT CARBOHYD 1127 1127  
 FT CARBOHYD 1128 1128  
 FT CARBOHYD 1129 1129  
 FT CARBOHYD 1130 1130  
 FT CARBOHYD 1131 1131  
 FT CARBOHYD 1132 1132  
 FT CARBOHYD 1133 1133  
 FT CARBOHYD 1134 1134  
 FT CARBOHYD 1135 1135  
 FT CARBOHYD 1136 1136  
 FT CARBOHYD 1137 1137  
 FT CARBOHYD 1138 1138  
 FT CARBOHYD 1139 1139  
 FT CARBOHYD 1140 1140  
 FT CARBOHYD 1141 1141  
 FT CARBOHYD 1142 1142  
 FT CARBOHYD 1143 1143  
 FT CARBOHYD 1144 1144  
 FT CARBOHYD 1145 1145  
 FT CARBOHYD 1146 1146  
 FT CARBOHYD 1147 1147  
 FT CARBOHYD 1148 1148  
 FT CARBOHYD 1149 1149  
 FT CARBOHYD 1150 1150  
 FT CARBOHYD 1151 1151  
 FT CARBOHYD 1152 1152  
 FT CARBOHYD 1153 1153  
 FT CARBOHYD 1154 1154  
 FT CARBOHYD 1155 1155  
 FT CARBOHYD 1156 1156  
 FT CARBOHYD 1157 1157  
 FT CARBOHYD 1158 1158  
 FT CARBOHYD 1159 1159  
 FT CARBOHYD 1160 1160  
 FT CARBOHYD 1161 1161  
 FT CARBOHYD 1162 1162  
 FT CARBOHYD 1163 1163  
 FT CARBOHYD 1164 1164  
 FT CARBOHYD 1165 1165  
 FT CARBOHYD 1166 1166  
 FT CARBOHYD 1167 1167  
 FT CARBOHYD 1168 1168  
 FT CARBOHYD 1169 1169  
 FT CARBOHYD 1170 1170  
 FT CARBOHYD 1171 1171  
 FT CARBOHYD 1172 1172  
 FT CARBOHYD 1173 1173  
 FT CARBOHYD 1174 1174  
 FT CARBOHYD 1175 1175  
 FT CARBOHYD 1176 1176  
 FT CARBOHYD 1177 1177  
 FT CARBOHYD 1178 1178  
 FT CARBOHYD 1179 1179  
 FT CARBOHYD 1180 1180  
 FT CARBOHYD 1

alignment of Seq. 4

RESULT 1  
US-09-245-808-1  
; Sequence 1, Application US/09245808  
; Patent No. 6313277  
; GENERAL INFORMATION:  
; APPLICANT: Doyle, L. Austin  
; APPLICANT: Abruzzo, Lynne V.  
; APPLICANT: Ross, Douglas D.  
; TITLE OF INVENTION: Breast Cancer Resistance Protein (BCRP) and DNA which  
; TITLE OF INVENTION: encodes it  
; FILE REFERENCE: Ross Umb conversion  
; CURRENT APPLICATION NUMBER: US/09/245,808  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: 60/073763  
; EARLIER FILING DATE: 1998-02-05  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 655  
; TYPE: PRT  
; ORGANISM: Human MCF-7/AdrVp cells  
US-09-245-808-1

Query Match 81.0%; Score 623; DB 4; Length 655;  
Best Local Similarity 81.6%; Pred. No. 1.9e-62;  
Matches 120; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

```
Qy      1 PGLGARAYTASSMALAIATGQSVVSVATLLMTIAFVFMMLFSGLLVNLRTIGPWLWLO 60
          | 4 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      511 FTLMMVAYSASSMALAIAAGQSVVSVATLLMTICFVFMMPFSGLLVNLTTIASWLSWLO 570

Qy      61 PSIPRYGFTALQYNEFLGQEFCEGFGNVTDNSTCVNSYAICTGNEYLINQGIELSPWGLWK 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      571 PSIPRYGFTALQHNEFLGQNFCEPGLNATGNNPC--NYATCTGEEYLVKQIDLSPWGLWK 628

Qy      121 NHVALACMIIFLTIAYLKLLFLKKYS 147
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      629 NHVALACMIVIFLTIAYLKLLFLKKYS 655
```

RESULT 2  
US-09-767-594-1  
; Sequence 1, Application US/09767594  
; Patent No. 6521635  
; GENERAL INFORMATION:  
; APPLICANT: Bates, Susan  
; APPLICANT: Robey, Robert  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by the Secretary of the  
; APPLICANT: Department of Health and Human Services